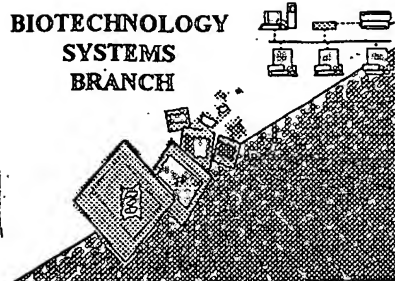


0580
0420

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/006,069
Source: OIPK
Date Processed by STIC: 12/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
Arlington, VA 22202

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 10/006,069

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) . . .
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/10/006,069

TIME: 10:39:51

Input Set : A:\194965830.app

Output Set: N:\CRF3\12172001\J006069.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Rebar, Edward
 5 Jamieson, Andrew
 6 Liu, Qiang
 7 Liu, Pei-Qi
 8 Wolffe, Alan
 9 Eisenberg, Stephen P.
 10 Jarvis, Eric
 11 Sangamo BioSciences, Inc.
 13 <120> TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
 14 Finger Proteins
 16 <130> FILE REFERENCE: 019496-005830US
 18 <140> CURRENT APPLICATION NUMBER: US/10/006,069
 19 <141> CURRENT FILING DATE: 2001-12-06
 21 <150> PRIOR APPLICATION NUMBER: US 09/733,604
 22 <151> PRIOR FILING DATE: 2000-12-07
 24 <150> PRIOR APPLICATION NUMBER: US 09/736,083
 25 <151> PRIOR FILING DATE: 2000-12-12
 27 <150> PRIOR APPLICATION NUMBER: US 09/846,033
 28 <151> PRIOR FILING DATE: 2001-04-30
 30 <160> NUMBER OF SEQ ID NOS: 252
 32 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

2464 <210> SEQ ID NO: 207
 2465 <211> LENGTH: 19
 2466 <212> TYPE: DNA
 2467 <213> ORGANISM: Artificial Sequence
 2469 <220> FEATURE:
 2470 <223> OTHER INFORMATION: target
 2472 <400> SEQUENCE: 207
 E--> 2473 **tgagcggcg cagcggagc**
 2916 <210> SEQ ID NO: 240
 2917 <211> LENGTH: 10
 2918 <212> TYPE: DNA
 2919 <213> ORGANISM: Artificial Sequence
 2921 <220> FEATURE:
 2922 <223> OTHER INFORMATION: target
 2924 <400> SEQUENCE: 240
 E--> 2925 **gctggggg**

19 (10)

(9) 10

see next page for more errors

<210> 4
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> target

<400> 4

ggggggaggn

9

see item 9 on Eva Summary Sheet

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,069

DATE: 12/17/2001

TIME: 10:39:52

Input Set : A:\194965830.app

Output Set: N:\CRF3\12172001\J006069.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:76 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
 L:76 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
 L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
 L:285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
 L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:2462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
 L:2473 M:254 E: No. of Bases conflict, LENGTH:Input:10 Counted:19 SEQ:207
 L:2499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:208
 L:2501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:208
 L:2775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:228
 L:2816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:231
 L:2857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:234
 L:2925 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:10 SEQ:240
